CLAIMS

Sub A1

1. A method of detecting and analysing differences between nucleic acids from two sources, which method comprises:

a. providing nucleic acids from two sources as labelled probes;

b. forming a mixture of the labelled probes with pooled reagents wherein each reagent is a population of beads carrying a polynucleotide target, the target of one reagent being different from the target of another reagent, the beads of one reagent being distinguishable from the beads of another reagent;

c. incubating the mixture under conditions to promote specific hybridisation between probes and targets; and,

d. analysing beads in the mixture by flow cytometry.

2. The method of claim 1 wherein the nucleic acids from two sources are mRNA or cDNA from cells or tissues.

Sub A2

3. The method of claim 1 or claim 2 wherein the polynucleotide targets are cDNA derived from cellular mRNA.

4. The method of any one of claims 1 to 3 wherein the polynucleotide targets are PCR amplimers.

5. The method of any one of claims 1 to 4 wherein the polynucleotide targets carry terminal biotin groups through which they are attached to streptavidin-coated beads.

6. The method of any one of claims 1 to 5 wherein the polynucleotide targets are single-stranded nucleic acids.

7. The method of any one of claims 1 to 6 wherein the labelled probes are single-stranded nucleic acids.

8. The method of any one of claims 1 to 7 wherein beads of one reagent are distinguishable from beads of another reagent by size.

9. The method of any one of claims 1 to 8 wherein beads of one reagent are distinguishable from beads of another reagent by the nature of the markers attached to the beads.

10. The method of any one of claims 1 to 9 wherein beads of one reagent are distinguishable from beads of another reagent by the concentration of markers attached to the beads.

11. The method of any one of claims 1 to 7 wherein beads of one reagent are distinguishable from beads of another reagent by size and/or by the nature and/or the concentration of markers attached to the beads.

12. The method of any one of claims 8 to 11 wherein fluorescent markers are attached to the beads.

13. The method of claim 1 or claim 2 wherein each probe is labelled with a fluorescent tag to indicate its source.

14. The method of any one of claims 1 to 13 wherein analysis by flow cytometry is performed to identify each bead and to quantify the probes bound thereto.

15. The method of any one of claims 1 to 14 wherein data obtained by flow cytometry is analysed to yield information about the relative and/or absolute abundances of individual sequences of the nucleic acids from the two sources.

Add A3